FIG. 1A

```
1   GGATAAGCCT GGGGCCAGCA TGAGCCAGAG GGAGGGAAGT CTGGAAGACC
    CCTATTCGGA CCCCGGTCGT ACTCGGTCTC CCTCCCTTCA GACCTTCTGG
1                            M   S   Q   R   E   G   S   L   E   D   H

51  ACCAGACTGA CTCCTCAATC TCATTCCTAC CCCATTTGGA GGCCAAGATC
    TGGTCTGACT GAGGAGTTAG AGTAAGGATG GGGTAAACCT CCGGTTCTAG
12   Q   T   D   S   S   I   S   F   L   P   H   L   E   A   K   I

101 CGCCAGACAC ACAACCTTGC CCGCCTCCTG ACCAAATATG CAGAACAACT
    GCGGTCTGTG TGTTGGAACG GGCGGAGGAC TGGTTTATAC GTCTTGTTGA
28  R   Q   T   H   N   L   A   R   L   L   T   K   Y   A   E   Q   L

151 TCTGGAGGAA TACGTGCAGC AACAGGGAGA GCCCTTTGGG CTGCCGGGCT
    AGACCTCCTT ATGCACGTCG TTGTCCCTCT CGGGAAACCC GACGGCCCGA
45   L   E   E   Y   V   Q   Q   Q   G   E   P   F   G   L   P   G   F

201 TCTCACCACC GCGGCTGCCG CTGGCCGGCC TGAGTGGCCC GGCTCCGAGC
    AGAGTGGTGG CGCCGACGGC GACCGGCCGG ACTCACCGGG CCGAGGCTCG
62   S   P   P   R   L   P   L   A   G   L   S   G   P   A   P   S

251 CATGCAGGGC TACCGGTGTC CGAGCGGCTG CGGCAGGATG CAGCCGCCCT
    GTACGTCCCG ATGGCCACAG GCTCGCCGAC GCCGTCCTAC GTCGGCGGGA
78  H   A   G   L   P   V   S   E   R   L   R   Q   D   A   A   A   L

301 GAGTGTGCTG CCCGCGCTGT TGGATGCCGT CCGCCGCCGC CAGGCGGAGC
    CTCACACGAC GGGCGCGACA ACCTACGGCA GGCGGCGGCG GTCCGCCTCG
95   S   V   L   P   A   L   L   D   A   V   R   R   R   Q   A   E   L

351 TGAACCCGCG CGCCCCGCGC CTGCTGCGGA GCCTGGAGGA CGCAGCCCGC
    ACTTGGGCGC GCGGGGCGCG GACGACGCCT CGGACCTCCT GCGTCGGGCG
112  N   P   R   A   P   R   L   L   R   S   L   E   D   A   A   R

401 CAGGTTCGGG CCCTGGGCGC CGCGGTGGAG ACAGTGCTGG CCGCGCTGGG
    GTCCAAGCCC GGGACCCGCG GCGCCACCTC TGTCACGACC GGCGCGACCC
128 Q   V   R   A   L   G   A   A   V   E   T   V   L   A   A   L   G

451 CGCTGCAGCC CGCGGGCCCG GGCCAGAGCC CGTCACCGTC GCCACCCTCT
    GCGACGTCGG GCGCCCGGGC CCGGTCTCGG GCAGTGGCAG CGGTGGGAGA
145  A   A   A   R   G   P   G   P   E   P   V   T   V   A   T   L   F

501 TCACGGCCAA CAGCACTGCA GGCATCTTCT CAGCCAAGGT GCTGGGGTTC
    AGTGCCGGTT GTCGTGACGT CCGTAGAAGA GTCGGTTCCA CGACCCCAAG
162  T   A   N   S   T   A   G   I   F   S   A   K   V   L   G   F

551 CACGTGTGCG GCCTCTATGG CGAGTGGGTG AGCCGCACAG AGGGCGACCT
    GTGCACACGC CGGAGATACC GCTCACCCAC TCGGCGTGTC TCCCGCTGGA
178 H   V   C   G   L   Y   G   E   W   V   S   R   T   E   G   D   L

601 GGGCCAGCTG GTGCCAGGGG GCGTCGCCTG AGAGTGAATA CTTTTTCTTG
    CCCGGTCGAC CACGGTCCCC CGCAGCGGAC TCTCACTTAT GAAAAAGAAC
195  G   Q   L   V   P   G   G   V   A   O
```

FIG. 1B

```
651  TAAGCTCGCT CTGTCTCGCC TCTTTGGCTT CAAATTTTCT GTCTCTCCAT
     ATTCGAGCGA GACAGAGCGG AGAAACCGAA GTTTAAAAGA CAGAGAGGTA

701  CTGTGTCCTG TGTGTTCTTG GGCTGTCCCT ATCTTTCTGC ATTTGTGTGG
     GACACAGGAC ACACAAGAAC CCGACAGGGA TAGAAAGACG TAAACACACC

751  TCTCTCTCTT CTGCTCTCCT CTCTGCAGGG AGCTTCTTTT TTCCAACAGT
     AGAGAGAGAA GACGAGAGGA GAGACGTCCC TCGAAGAAAA AAGGTTGTCA

801  TTCTCGTTTT GTCTCTCTCC AGTCTTGAAC ACTTTTGTCT CCGAGAGGTC
     AAGAGCAAAA CAGAGAGAGG TCAGAACTTG TGAAAACAGA GGCTCTCCAG

851  TCTTTTTGTT TCCTTGTCTC TTGGTTCTTT CTTTGCTTGC TTGCTTGCTT
     AGAAAAACAA AGGAACAGAG AACCAAGAAA GAAACGAACG AACGAACGAA

901  GCTTGCTTGT TGTTGAGACA GGGTCTCACC ATATAGCTCT GGATGGCCTG
     CGAACGAACA ACAACTCTGT CCCAGAGTGG TATATCGAGA CCTACCGGAC

951  GAACTTGCTA TGTAGGCCAG GCTGGCCTCC AGCTCATAGA GATCCACTTG
     CTTGAACGAT ACATCCGGTC CGACCGGAGG TCGAGTATCT CTAGGTGAAC

1001 CCTCCGACTC CCAATTTCCC CATCTGTCTC CCTGTGATCC ATATGGGTAT
     GGAGGCTGAG GGTTAAAGGG GTAGACAGAG GGACACTAGG TATACCCATA

1051 GTGTAACCCT TACTTTGTCT CATGGAGGTG ACAATTTTTC TCCCTTCAGT
     CACATTGGGA ATGAAACAGA GTACCTCCAC TGTTAAAAAG AGGGAAGTCA

1101 TTCTTTGTTC TTTACTGACC AGAAAAGTGC CTACTTGTCC CCTGGTGGCA
     AAGAAACAAG AAATGACTGG TCTTTTCACG GATGAACAGG GGACCACCGT

1151 AGGCCATTCA CCTTAGGACC TTCCCACCAG TTCCTTTGTA GGCAAATCCC
     TCCGGTAAGT GGAATCCTGG AAGGGTGGTC AAGGAAACAT CCGTTTAGGG

1201 TCCCCCTTTG AGGTCCTTCC CTTTCATACC GCCCTAGGCT GGTCAATGGA
     AGGGGGAAAC TCCAGGAAGG GAAAGTATGG CGGGATCCGA CCAGTTACCT

1251 GAGAGAAAGG CAGAAAAACA TCTTTAAAGA GTTTTATTTG AGAATAAATT
     CTCTCTTTCC GTCTTTTTGT AGAAATTTCT CAAAATAAAC TCTTATTTAA

1301 AATTTTTGTA AATAAAATGT TTAACAATAA AACTAAACTT TTATGAAAAA
     TTAAAAACAT TTATTTTACA AATTGTTATT TTGATTTGAA AATACTTTTT

1351 AA (polyA)
     TT
```

FIG. 2

```
                  10        20        30        40        50
chf.781   MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQ
                              **          ***        * * **
humcntf             MAFTEHSPLTPHRRDLCSRSIWLARKIRSDLTALTESYVK
                            10        20        30        40

                  60        70        80        90       100
chf.781   QQGEPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPAL
           **        *    * *               ***     *      *
humcntf   HQGLNKNINLDSADGMPVA----STDQWSELTEAERLQENLQAYRTFHVL
                  50            60        70        80

                  110       120       130       140
chf.781   LD-AVRRRQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARG
          *       *    *              ** *     *     *
humcntf   LARLLEDQQVHFTPTEGDFHQAIHTLLLQVAAFAYQIEELMILLEYKIPR
            90       100       110       120       130

        150       160       170       180       190
chf.781   PGPEPVTVATLFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVP
                            * *  *  *  *      *  *   **
humcntf   NEADGMPINV-----GDGGLFEKKLWGLKVLQELSQWTVRSIHDL-RFIS
           140            150       160       170        180

        200
chf.781   GGVAO

humcntf   SHQTGIPARGSHYIANNKKM
                  190       200
```

FIG. 3

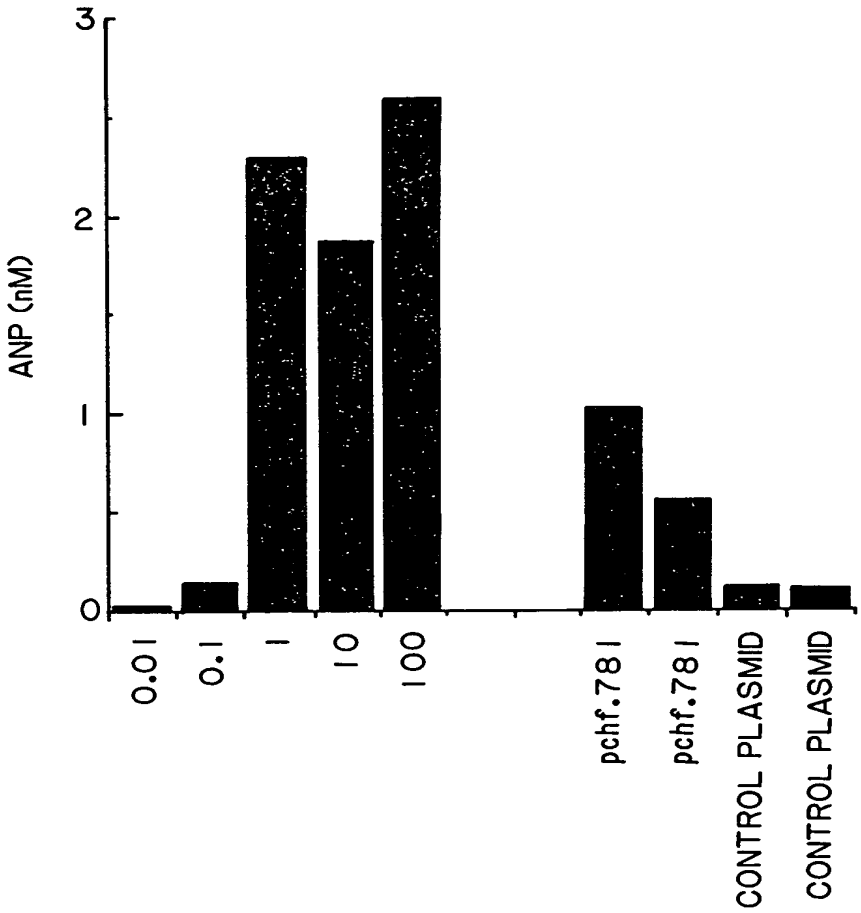
3
2
1
0
ANP (nM)
0.01
0.1
1
10
100
pchf.781
pchf.781
CONTROL PLASMID
CONTROL PLASMID
PHENYLEPHRINE (uM)
STANDARD CURVE
293 TRANSFECTION

FIG. 4

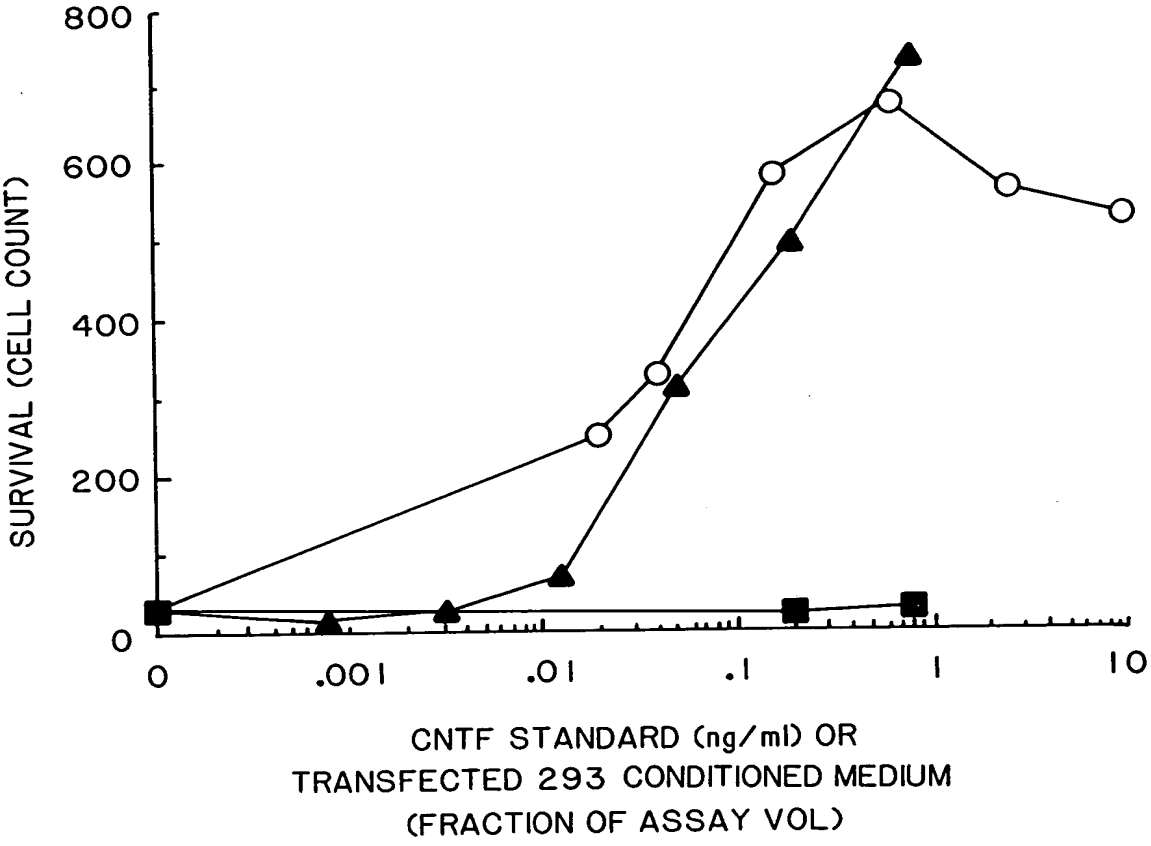
800
600
400
200
0
SURVIVAL (CELL COUNT)
0
.001
.01
.1
1
10
CNTF STANDARD (ng/ml) OR
TRANSFECTED 293 CONDITIONED MEDIUM
(FRACTION OF ASSAY VOL)

FIG. 5A

```
1    GTGAAGGGAG CCGGGATCAG CCAGGGGCCA GCATGAGCCG GAGGGAGGGA
     CACTTCCCTC GGCCCTAGTC GGTCCCCGGT CGTACTCGGC CTCCCTCCCT
1                                         M  S  R  R  E  G

51   AGTCTGGAAG ACCCCCAGAC TGATTCCTCA GTCTCACTTC TTCCCCACTT
     TCAGACCTTC TGGGGGTCTG ACTAAGGAGT CAGAGTGAAG AAGGGGTGAA
7    S  L  E  D  P  Q  T  D  S  S  V  S  L  L  P  H  L

101  GGAGGCCAAG ATCCGTCAGA CACACAGCCT TGCGCACCTC CTCACCAAAT
     CCTCCGGTTC TAGGCAGTCT GTGTGTCGGA ACGCGTGGAG GAGTGGTTTA
24    E  A  K  I  R  Q  T  H  S  L  A  H  L  L  T  K  Y

151  ACGCTGAGCA GCTGCTCCAG GAATATGTGC AGCTCCAGGG AGACCCCTTC
     TGCGACTCGT CGACGAGGTC CTTATACACG TCGAGGTCCC TCTGGGGAAG
41    A  E  Q  L  L  Q  E  Y  V  Q  L  Q  G  D  P  F

201  GGGCTGCCCA GCTTCTCGCC GCCGCGGCTG CCGGTGGCCG GCCTGAGCGC
     CCCGACGGGT CGAAGAGCGG CGGCGCCGAC GGCCACCGGC CGGACTCGCG
57   G  L  P  S  F  S  P  P  R  L  P  V  A  G  L  S  A

251  CCCGGCTCCG AGCCACGCGG GGCTGCCAGT GCACGAGCGG CTGCGGCTGG
     GGGCCGAGGC TCGGTGCGCC CCGACGGTCA CGTGCTCGCC GACGCCGACC
74    P  A  P  S  H  A  G  L  P  V  H  E  R  L  R  L  D

301  ACGCGGCGGC GCTGGCCGCG CTGCCCCCGC TGCTGGACGC AGTGTGTCGC
     TGCGCCGCCG CGACCGGCGC GACGGGGGCG ACGACCTGCG TCACACAGCG
91     A  A  A  L  A  A  L  P  P  L  L  D  A  V  C  R

351  CGCCAGGCCG AGCTGAACCC GCGCGCGCCG CGCCTGCTGC GCCGCCTGGA
     GCGGTCCGGC TCGACTTGGG CGCGCGCGGC GCGGACGACG CGGCGGACCT
107  R  Q  A  E  L  N  P  R  A  P  R  L  L  R  R  L  E

401  GGACGCGGCG CGCCAGGCCC GGGCCCTGGG CGCCGCCGTG GAGGCCTTGC
     CCTGCGCCGC GCGGTCCGGG CCCGGGACCC GCGGCGGCAC CTCCGGAACG
124   D  A  A  R  Q  A  R  A  L  G  A  A  V  E  A  L  L

451  TGGCCGCGCT GGGCGCCGCC AACCGCGGGC CCCGGGCCGA GCCCCCCGCC
     ACCGGCGCGA CCCGCGGCGG TTGGCGCCCG GGGCCCGGCT CGGGGGGCGG
141   A  A  L  G  A  A  N  R  G  P  R  A  E  P  P  A
```

FIG. 5B

```
501   GCCACCGCCT CAGCCGCCTC CGCCACCGGG GTCTTCCCCG CCAAGGTGCT
      CGGTGGCGGA GTCGGCGGAG GCGGTGGCCC CAGAAGGGGC GGTTCCACGA
157   A  T  A  S   A  A  S   A  T  G   V  F  P  A   K  V  L

551   GGGGCTCCGC GTTTGCGGCC TCTACCGCGA GTGGCTGAGC CGCACCGAGG
      CCCCGAGGCG CAAACGCCGG AGATGGCGCT CACCGACTCG GCGTGGCTCC
174    G  L  R   V  C  G  L   Y  R  E   W  L  S   R  T  E  G

601   GCGACCTGGG CCAGCTGCTG CCCGGGGGCT CGGCCTGAGC GCCGCGGGGC
      CGCTGGACCC GGTCGACGAC GGGCCCCCGA GCCGGACTCG CGGCGCCCCG
191    D  L  G   Q  L  L   P  G  G  S   A  O

651   AGCTCGCCCC GCCTCCTCCC GCTGGGTTCC GTCTCTCCTT CCGCTTCTTT
      TCGAGCGGGG CGGAGGAGGG CGACCCAAGG CAGAGAGGAA GGCGAAGAAA

701   GTCTTTCTCT GCCGCTGTCG GTGTCTGTCT GTCTGCTCTT AGCTGTCTCC
      CAGAAAGAGA CGGCGACAGC CACAGACAGA CAGACGAGAA TCGACAGAGG

751   ATTGCCTCGG CCTTCTTTGC TTTTTGTGGG GGAGAGGGGA GGGGACGGGC
      TAACGGAGCC GGAAGAAACG AAAAACACCC CCTCTCCCCT CCCCTGCCCG

801   AGGGTCTCTG TCGCCCAGGC TGGGGTGCAG TGGCGCGATC CCAGCACTGC
      TCCCAGAGAC AGCGGGTCCG ACCCCACGTC ACCGCGCTAG GGTCGTGACG

851   AGCCTCAACC TCCTGGGCTC AAGCCATCCT TCCGCCTCAG CTTCCCCAGC
      TCGGAGTTGG AGGACCCGAG TTCGGTAGGA AGGCGGAGTC GAAGGGGTCG

901   AGCTGGGACT ACAGGCACGC GCCACCACAG CCGGCTAATT TTTTATTTAA
      TCGACCCTGA TGTCCGTGCG CGGTGGTGTC GGCCGATTAA AAAATAAATT

951   TTTTTTGTAG AGACGAGGTT TCGCCATGTT GCCCAGGCTG GTCTTGAACT
      AAAAAACATC TCTGCTCCAA AGCGGTACAA CGGGTCCGAC CAGAACTTGA

1001  CCGGGGCTCA AGCGATCC
      GGCCCCGAGT TCGCTAGG
```

FIG. 6

```
humct1      1  MSRREGSLEDPQTDSSVSLLPHLEAKIRQTHSLAHLLTKYAEQLLQEYVQLQG
               ** ******* ***** * ************ ** ********** **** **
chf.781     1  MSQREGSLEDHQTDSSISFLPHLEAKIRQTHNLARLLTKYAEQLLEEYVQQQG

humct1     54 DPFGLPSFSPPRLPVAGLSAPAPSHAGLPVHERLRLDAAALAALPPLLDAVCR
               ***** ******* **** ********** **** *****  ** ***** *
chf.781    54 EPFGLPGFSPPRLPLAGLSGPAPSHAGLPVSERLRQDAAALSVLPALLDAVRR

humct1    107 RQAELNPRAPRLLRRLEDAARQARALGAAVEALLAALGAANRGPRAEPPAATA
               ************** ******* ********  ******* ***  **
chf.781   107 RQAELNPRAPRLLRSLEDAARQVRALGAAVETVLAALGAAARGPGPEPVTVAT

humct1    160 --SAASATGVFPAKVLGLRVCGLYREWLSRTEGDLGQLLPGGSA
                 * *  * * *****  ***** ** ********** *** *
chf.781   160 LFTANSTAGIFSAKVLGFHVCGLYGEWVSRTEGDLGQLVPGGVA
```